Hayes, R.

1644

ENTERED

RAW SEQUENCE LISTING   DATE: 05/01/2000
PATENT APPLICATION: **US/09/224,556**   TIME: 08:19:50

Input Set : **A:\templst.txt**
Output Set: **N:\CRF3\050100\I224556.raw**

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 4 <110> APPLICANT: Dixit, Vishva M.
 6 <120> TITLE OF INVENTION: CD40 BINDING COMPOSITIONS AND METHODS OF
 7       USING SAME
 9 <130> FILE REFERENCE: 128019201702
11 <140> CURRENT APPLICATION NUMBER: 09/224,556
12 <141> CURRENT FILING DATE: 1998-12-30
14 <150> PRIOR APPLICATION NUMBER: 08/826,577
15 <151> PRIOR FILING DATE: 1997-04-02
17 <150> PRIOR APPLICATION NUMBER: 08/404,832
18 <151> PRIOR FILING DATE: 1995-03-13
20 <160> NUMBER OF SEQ ID NOS: 16
22 <170> SOFTWARE: FastSEQ for Windows Version 3.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 2339
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (211)...(1911)
33 <400> SEQUENCE: 1
34 acgaaggcca cgcgcccggc gcccctgagc cggccgagcg gcgacggacc gcgagatgag    60
35 gaaaatgagg cccaaagaag tgatgccact tggttaaggt cccagagcag gtcagaatca   120
36 gacctaggat cagaaacctg gctcctggct cctgctccct actcttctaa ggatcgctgt   180
37 cctgacagaa gagaactcct ctttcctaaa atg gag tcg agt aaa aag atg gac   234
38                                     Met Glu Ser Ser Lys Lys Met Asp
39                                      1               5
41 tct cct ggc gcg ctg cag act aac ccg ccg cta aag ctg cac act gac   282
42 Ser Pro Gly Ala Leu Gln Thr Asn Pro Pro Leu Lys Leu His Thr Asp
43         10              15                  20
45 cgc agt gct ggg acg cca gtt ttt gtc cct gaa caa gga ggt tac aag   330
46 Arg Ser Ala Gly Thr Pro Val Phe Val Pro Glu Gln Gly Gly Tyr Lys
47  25              30                  35                  40
49 gaa aag ttt gtg aag acc gtg gag gac aag tac aag tgt gag aag tgc   378
50 Glu Lys Phe Val Lys Thr Val Glu Asp Lys Tyr Lys Cys Glu Lys Cys
51              45                  50                  55
53 cac ctg gtg ctg tgc agc ccg aag cag acc gag tgt ggg cac cgc ttc   426
54 His Leu Val Leu Cys Ser Pro Lys Gln Thr Glu Cys Gly His Arg Phe
55              60                  65                  70
57 tgc gag agc tgc atg gcg gcc ctg ctg agc tct tca agt cca aaa tgt   474
58 Cys Glu Ser Cys Met Ala Ala Leu Leu Ser Ser Ser Ser Pro Lys Cys
59          75                  80                  85
61 aca gcg tgt caa gag agc atc gtt aaa gat aag gtg ttt aag gat aat   522
62 Thr Ala Cys Gln Glu Ser Ile Val Lys Asp Lys Val Phe Lys Asp Asn
63          90                  95                  100
65 tgc tgc aag aga gaa att ctg gct ctt cag atc tat tgt cgg aat gaa   570
66 Cys Cys Lys Arg Glu Ile Leu Ala Leu Gln Ile Tyr Cys Arg Asn Glu
67 105                 110                 115                 120
```

RECEIVED JUN 07 2000 TECH CENTER 1600/2900

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```
69   agc aga ggt tgt gca gag cag tta atg ctg gga cat ctg gtg cat tta     618
70   Ser Arg Gly Cys Ala Glu Gln Leu Met Leu Gly His Leu Val His Leu
71               125                 130                 135
73   aaa aat gat tgc cat ttt gaa gaa ctt cca tgt gtg cgt cct gac tgc     666
74   Lys Asn Asp Cys His Phe Glu Glu Leu Pro Cys Val Arg Pro Asp Cys
75               140                 145                 150
77   aaa gaa aag gtc ttg agg aaa gac ctg cga gac cac gtg gag aag gcg     714
78   Lys Glu Lys Val Leu Arg Lys Asp Leu Arg Asp His Val Glu Lys Ala
79               155                 160                 165
81   tgt aaa tac cgg gaa gcc aca tgc agc cac tgc aag agt cag gtt ccg     762
82   Cys Lys Tyr Arg Glu Ala Thr Cys Ser His Cys Lys Ser Gln Val Pro
83         170                 175                 180
85   atg atc gcg ctg cag aaa cac gaa gac acc gac tgt ccc tgc gtg gtg     810
86   Met Ile Ala Leu Gln Lys His Glu Asp Thr Asp Cys Pro Cys Val Val
87   185                 190                 195                 200
89   gtg tcc tgc cct cac aag tgc agc gtc cag act ctc ctg agg agc gag     858
90   Val Ser Cys Pro His Lys Cys Ser Val Gln Thr Leu Leu Arg Ser Glu
91               205                 210                 215
93   ttg agt gca cac ttg tca gag tgt gtc aat gcc ccc agc acc tgt agt     906
94   Leu Ser Ala His Leu Ser Glu Cys Val Asn Ala Pro Ser Thr Cys Ser
95               220                 225                 230
97   ttt aag cgc tat ggc tgc gtt ttt cag ggg aca aac cag cag atc aag     954
98   Phe Lys Arg Tyr Gly Cys Val Phe Gln Gly Thr Asn Gln Gln Ile Lys
99               235                 240                 245
101  gcc cac gag gca agc tcc gcc gtg cag cac gtc aac ctg ctg aag gag     1002
102  Ala His Glu Ala Ser Ser Ala Val Gln His Val Asn Leu Leu Lys Glu
103         250                 255                 260
105  tgg agc aac tcg ctc gaa aag aag gtt tcc ttg ttg cag aat gaa agt     1050
106  Trp Ser Asn Ser Leu Glu Lys Lys Val Ser Leu Leu Gln Asn Glu Ser
107  265                 270                 275                 280
109  gta gaa aaa aac aag agc ata caa agt ttg cac aat cag ata tgt agc     1098
110  Val Glu Lys Asn Lys Ser Ile Gln Ser Leu His Asn Gln Ile Cys Ser
111               285                 290                 295
113  ttt gaa att gaa att gag aga caa aag gaa atg ctt cga aat aat gaa     1146
114  Phe Glu Ile Glu Ile Glu Arg Gln Lys Glu Met Leu Arg Asn Asn Glu
115               300                 305                 310
117  tcc aaa atc ctt cat tta cag cga gtg ata gac agc caa gca gag aaa     1194
118  Ser Lys Ile Leu His Leu Gln Arg Val Ile Asp Ser Gln Ala Glu Lys
119         315                 320                 325
121  ctg aag gag ctt gac aag gag atc cgg ccc ttc cgg cag aac tgg gag     1242
122  Leu Lys Glu Leu Asp Lys Glu Ile Arg Pro Phe Arg Gln Asn Trp Glu
123         330                 335                 340
125  gaa gca gac agc atg aag agc agc gtg gag tcc ctc cag aac cgc gtg     1290
126  Glu Ala Asp Ser Met Lys Ser Ser Val Glu Ser Leu Gln Asn Arg Val
127  345                 350                 355                 360
129  acc gag ctg gag agc gtg gac aag agc gcg ggg caa gtg gct cgg aac     1338
130  Thr Glu Leu Glu Ser Val Asp Lys Ser Ala Gly Gln Val Ala Arg Asn
131               365                 370                 375
133  aca ggc ctg ctg gag tcc cag ctg agc cgg cat gac cag atg ctg agt     1386
```

```
134  Thr Gly Leu Leu Glu Ser Gln Leu Ser Arg His Asp Gln Met Leu Ser
135          380                 385                 390
137  gtg cac gac atc cgc cta gcc gac atg gac ctg ggc ttc cag gtc ctg     1434
138  Val His Asp Ile Arg Leu Ala Asp Met Asp Leu Gly Phe Gln Val Leu
139          395                 400                 405
141  gag acc gcc agc tac aat gga gtg ctc atc tgg aag att cgc gac tac     1482
142  Glu Thr Ala Ser Tyr Asn Gly Val Leu Ile Trp Lys Ile Arg Asp Tyr
143      410                 415                 420
145  aag cgg cgg aag cag gag gcc gtc atg ggg aag acc ctg tcc ctt tac     1530
146  Lys Arg Arg Lys Gln Glu Ala Val Met Gly Lys Thr Leu Ser Leu Tyr
147  425                 430                 435                 440
149  agc cag cct ttc tac act ggt tac ttt ggc tat aag atg tgt gcc agg     1578
150  Ser Gln Pro Phe Tyr Thr Gly Tyr Phe Gly Tyr Lys Met Cys Ala Arg
151              445                 450                 455
153  gtc tac ctg aac ggg gac ggg atg ggg aag ggg acg cac ttg tcg ctg     1626
154  Val Tyr Leu Asn Gly Asp Gly Met Gly Lys Gly Thr His Leu Ser Leu
155              460                 465                 470
157  ttt ttt gtc atc atg cgt gga gaa tat gat gcc ctg ctt cct tgg ccg     1674
158  Phe Phe Val Ile Met Arg Gly Glu Tyr Asp Ala Leu Leu Pro Trp Pro
159          475                 480                 485
161  ttt aag cag aaa gtg aca ctc atg ctg atg gat cag ggg tcc tct cga     1722
162  Phe Lys Gln Lys Val Thr Leu Met Leu Met Asp Gln Gly Ser Ser Arg
163      490                 495                 500
165  cgt cat ttg gga gat gca ttc aag ccc gac ccc aac agc agc agc ttc     1770
166  Arg His Leu Gly Asp Ala Phe Lys Pro Asp Pro Asn Ser Ser Ser Phe
167  505                 510                 515                 520
169  aag aag ccc act gga gag atg aat atc gcc tct ggc tgc cca gtc ttt     1818
170  Lys Lys Pro Thr Gly Glu Met Asn Ile Ala Ser Gly Cys Pro Val Phe
171              525                 530                 535
173  gtg gcc caa act gtt cta gaa aat ggg aca tat att aaa gat gat aca     1866
174  Val Ala Gln Thr Val Leu Glu Asn Gly Thr Tyr Ile Lys Asp Asp Thr
175              540                 545                 550
177  att ttt att aaa gtc ata gtg gat act tcg gat ctg ccc gat ccc         1911
178  Ile Phe Ile Lys Val Ile Val Asp Thr Ser Asp Leu Pro Asp Pro
179          555                 560                 565
181  tgataagtag ctggggaggt ggatttagca gaaggcaact cctctggggg atttgaaccg     1971
182  gtctgtcttc actgaggtcc tcgcgctcag aaaaggacct tgtgagacgg aggaagcggc     2031
183  agaaggcgga cgcgtgccgg cgggaggagc cacgcgagag cacacctgac acgttttata     2091
184  atagactagc cacacttcac tctgaagaat tatttatcct tcaacaagat aaatattgct     2151
185  gtcagagaag gttttcattt tcattttaa agatctagtt aattaaggtg gaaaacatat      2211
186  atgctaaaca aaagaaacat gattttctt ccttaaactt gaacaccaaa aaaacacaca       2271
187  cacacacaca cgtggggata gctggacatg tcagcatgtt aagtaaaagg agaatttatg     2331
188  aaatagta                                                              2339
190  <210> SEQ ID NO: 2
191  <211> LENGTH: 567
192  <212> TYPE: PRT
193  <213> ORGANISM: Homo sapiens
195  <400> SEQUENCE: 2
196  Met Glu Ser Ser Lys Lys Met Asp Ser Pro Gly Ala Leu Gln Thr Asn
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RAW SEQUENCE LISTING   DATE: 05/01/2000
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Input Set : A:\templst.txt
Output Set: N:\CRF3\050100\I224556.raw

```
197  1                   5                   10                  15
198  Pro Pro Leu Lys Leu His Thr Asp Arg Ser Ala Gly Thr Pro Val Phe
199              20                  25                  30
200  Val Pro Glu Gln Gly Gly Tyr Lys Glu Lys Phe Val Lys Thr Val Glu
201              35                  40                  45
202  Asp Lys Tyr Lys Cys Glu Lys Cys His Leu Val Leu Cys Ser Pro Lys
203      50                  55                  60
204  Gln Thr Glu Cys Gly His Arg Phe Cys Glu Ser Cys Met Ala Ala Leu
205  65                  70                  75                  80
206  Leu Ser Ser Ser Ser Pro Lys Cys Thr Ala Cys Gln Glu Ser Ile Val
207              85                  90                  95
208  Lys Asp Lys Val Phe Lys Asp Asn Cys Cys Lys Arg Glu Ile Leu Ala
209              100                 105                 110
210  Leu Gln Ile Tyr Cys Arg Asn Glu Ser Arg Gly Cys Ala Glu Gln Leu
211              115                 120                 125
212  Met Leu Gly His Leu Val His Leu Lys Asn Asp Cys His Phe Glu Glu
213      130                 135                 140
214  Leu Pro Cys Val Arg Pro Asp Cys Lys Glu Lys Val Leu Arg Lys Asp
215  145                 150                 155                 160
216  Leu Arg Asp His Val Glu Lys Ala Cys Lys Tyr Arg Glu Ala Thr Cys
217              165                 170                 175
218  Ser His Cys Lys Ser Gln Val Pro Met Ile Ala Leu Gln Lys His Glu
219              180                 185                 190
220  Asp Thr Asp Cys Pro Cys Val Val Val Ser Cys Pro His Lys Cys Ser
221      195                 200                 205
222  Val Gln Thr Leu Leu Arg Ser Glu Leu Ser Ala His Leu Ser Glu Cys
223      210                 215                 220
224  Val Asn Ala Pro Ser Thr Cys Ser Phe Lys Arg Tyr Gly Cys Val Phe
225  225                 230                 235                 240
226  Gln Gly Thr Asn Gln Gln Ile Lys Ala His Glu Ala Ser Ser Ala Val
227              245                 250                 255
228  Gln His Val Asn Leu Leu Lys Glu Trp Ser Asn Ser Leu Glu Lys Lys
229              260                 265                 270
230  Val Ser Leu Leu Gln Asn Glu Ser Val Glu Lys Asn Lys Ser Ile Gln
231      275                 280                 285
232  Ser Leu His Asn Gln Ile Cys Ser Phe Glu Ile Glu Ile Glu Arg Gln
233      290                 295                 300
234  Lys Glu Met Leu Arg Asn Asn Glu Ser Lys Ile Leu His Leu Gln Arg
235  305                 310                 315                 320
236  Val Ile Asp Ser Gln Ala Glu Lys Leu Lys Glu Leu Asp Lys Glu Ile
237              325                 330                 335
238  Arg Pro Phe Arg Gln Asn Trp Glu Glu Ala Asp Ser Met Lys Ser Ser
239              340                 345                 350
240  Val Glu Ser Leu Gln Asn Arg Val Thr Glu Leu Glu Ser Val Asp Lys
241              355                 360                 365
242  Ser Ala Gly Gln Val Ala Arg Asn Thr Gly Leu Leu Glu Ser Gln Leu
243      370                 375                 380
244  Ser Arg His Asp Gln Met Leu Ser Val His Asp Ile Arg Leu Ala Asp
245  385                 390                 395                 400
```

RAW SEQUENCE LISTING   DATE: 05/01/2000
PATENT APPLICATION: **US/09/224,556** TIME: 08:19:51

Input Set : **A:\templst.txt**
Output Set: **N:\CRF3\050100\I224556.raw**

```
246  Met Asp Leu Gly Phe Gln Val Leu Glu Thr Ala Ser Tyr Asn Gly Val
247                  405                 410                 415
248  Leu Ile Trp Lys Ile Arg Asp Tyr Lys Arg Arg Lys Gln Glu Ala Val
249                  420                 425                 430
250  Met Gly Lys Thr Leu Ser Leu Tyr Ser Gln Pro Phe Tyr Thr Gly Tyr
251                  435                 440                 445
252  Phe Gly Tyr Lys Met Cys Ala Arg Val Tyr Leu Asn Gly Asp Gly Met
253      450             455                 460
254  Gly Lys Gly Thr His Leu Ser Leu Phe Phe Val Ile Met Arg Gly Glu
255  465                 470                 475                 480
256  Tyr Asp Ala Leu Leu Pro Trp Pro Phe Lys Gln Lys Val Thr Leu Met
257                  485                 490                 495
258  Leu Met Asp Gln Gly Ser Ser Arg Arg His Leu Gly Asp Ala Phe Lys
259                  500                 505                 510
260  Pro Asp Pro Asn Ser Ser Ser Phe Lys Lys Pro Thr Gly Glu Met Asn
261              515                 520                 525
262  Ile Ala Ser Gly Cys Pro Val Phe Val Ala Gln Thr Val Leu Glu Asn
263      530             535                 540
264  Gly Thr Tyr Ile Lys Asp Asp Thr Ile Phe Ile Lys Val Ile Val Asp
265  545                 550                 555                 560
266  Thr Ser Asp Leu Pro Asp Pro
267                  565
269  <210> SEQ ID NO: 3
270  <211> LENGTH: 49
271  <212> TYPE: PRT
272  <213> ORGANISM: Homo sapiens
274  <400> SEQUENCE: 3
275  Asp Lys Tyr Lys Cys Glu Lys Cys His Leu Val Leu Cys Ser Pro Lys
276  1               5                   10                  15
277  Gln Thr Glu Cys Gly His Arg Phe Cys Glu Ser Cys Met Ala Ala Leu
278                  20                  25                  30
279  Leu Ser Ser Ser Ser Pro Lys Cys Thr Ala Cys Gln Glu Ser Ile Val
280              35                  40                  45
281  Lys
284  <210> SEQ ID NO: 4
285  <211> LENGTH: 50
286  <212> TYPE: PRT
287  <213> ORGANISM: Homo sapiens
289  <400> SEQUENCE: 4
290  Ala Lys Tyr Leu Cys Ser Ala Cys Lys Asn Ile Leu Arg Arg Pro Phe
291  1               5                   10                  15
292  Gln Ala Gln Cys Gly His Arg Tyr Cys Ser Phe Cys Leu Thr Ser Ile
293                  20                  25                  30
294  Leu Ser Ser Gly Pro Gln Asn Cys Ala Ala Cys Val Tyr Glu Gly Leu
295              35                  40                  45
296  Tyr Glu
297      50
299  <210> SEQ ID NO: 5
300  <211> LENGTH: 49
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